Listing of Claims:

The following listing of claims replaces all prior versions and listings of claims in the application.

1. (Previously presented) A full-length variant of the interferon gamma (IFNG) polypeptide of SEQ ID NO: 1, said variant exhibiting IFNG activity and consisting of up to 10 residue modifications from residues 1 through 131 of SEQ ID NO: 1, and

(a) at least one amino acid substitution in a position selected from the group consisting of S132 and S142; and

(b) at least one amino acid substitution in a position selected from the group consisting of R137, R139 and R140.

2. (Original) The full-length variant according to claim 1, wherein said amino acid substitution is selected from the group consisting of S132P, S142P and S132P+S142P.

3. (Original) The full-length variant according to claim 2, wherein said amino acid substitution is S132P.

4. (Original) The full-length variant according to claim 2, wherein said amino acid substitution is S142P.

5. (Previously presented) The full-length variant of claim 2, wherein at least one non-positively charged amino acid residue is introduced by substitution in a position selected from the group consisting of R137, R139 and R140.

6. (Original) The full-length variant according to claim 5, wherein said non-positively charged amino acid residue is a proline residue.

7. (Previously presented) The full-length variant of claim 5, wherein said variant comprises the following substitutions: R137P+R139P+S142P.

8. (Previously presented) The full-length variant of claim 5, wherein said variant comprises the following substitutions: R137P+S142P.

9. (Previously presented) The full-length variant of claim 5, wherein said variant comprises the following substitutions: S132P+R137P+R140P.

10. (Previously presented) The full-length variant of claim 5, wherein said variant comprises the following substitutions: S132P+R140P.

11. (Previously presented) A full-length variant of the interferon gamma (IFNG) polypeptide of SEQ ID NO: 1, said variant exhibiting IFNG activity and consisting of up to 10 residue modifications from residues 1 through 131 of SEQ ID NO: 1, an amino acid substitution in position R137 and an amino acid substitution in position R140.

12. (Original) The full-length variant according to claim 11, wherein said variant comprises the substitutions R137X+R140P, wherein X is any amino acid residue, except arginine and lysine.

13. (Original) The full-length variant according to claim 11, wherein said variant comprises the substitutions R137P+R140X, wherein X is any amino acid residue, except arginine.

14. (Previously presented) The full-length variant of claim 11, wherein said variant comprises the substitutions R137P+R140P.

15. (Previously presented) The full-length variant of claim 11, wherein said variant comprises at least one further modification in the C-terminal part from amino acid residue S132 to amino acid residue Q143.

16. (Original) The full-length variant according to claim 15, wherein said further modification comprises introduction of at least one cysteine residue.

17. (Original) The full-length variant according to claim 16, wherein said cysteine residue is covalently attached to a polymer molecule.

18. (Original) The full-length variant according to claim 17, where said polymer molecule is a linear or branched polyethylene glycol.

19. (Cancelled)

20. (Previously presented) The full-length variant according to claim 11, wherein said modifications are substitutions.

21. (Previously presented) The full-length variant according to claim 20, wherein said variant comprises the substitution S99T.

22. (Previously presented) The full-length variant of claim 1, wherein said up to 10 residue modifications from residues 1 through 131 comprises at least one introduced and/or at least one removed amino acid residue comprising an attachment group for a non-polypeptide moiety.

23. (Previously presented) The full-length variant according to claim 22, wherein said up to 10 residue modifications comprises at least one introduced glycosylation site.

24. (Original) The full-length variant according to claim 23, wherein said glycosylation site is an N-glycosylation site.

25. (Original) The full-length variant according to claim 24, wherein said N-glycosylation site is introduced in a position comprising an amino acid residue having at least 25% of its side chain exposed to the surface (as defined in Example 1 herein).

26. (Original) The full-length variant according to claim 25, wherein said N-glycosylation site is introduced in a position comprising an amino acid residue having at least 50% of its said chain exposed to the surface (as defined in Example 1 herein).

27. (Previously presented) The full-length variant of claim 24, wherein said N-glycosylation site is introduced by substitution.

28. (Currently amended) The full-length variant according to claim 1, wherein said up to 10 residue modifications is a substitution ~~is~~ selected from the group consisting of G18S, G18T, E38N, E38N+S40T, K61S, K61T, S65N+Q67S, S65N+Q67T, N85S, N85T, K94N, Q106S and Q106T.

29. (Original) The full-length variant according to claim 28, wherein said substitution is selected from the group consisting of G18T, E38N+S40T, K61T, S65N+Q67T, N85T, K94N and Q106T.

30. (Original) The full-length variant according to claim 29, wherein said substitution is selected from the group consisting of G18T, E38N+S40T, K61T, S65N+Q67T and N85T.

31. (Original) The full-length variant according to claim 30, wherein said substitution is E38N+S40T.

32. (Previously presented) The full-length variant according to claim 22, wherein said up to 10 residue modifications comprises an introduced cysteine residue.

33. (Currently amended) The full-length variant according to claim 32, wherein said cysteine residue is introduced in a position comprising an amino acid residue having at least 25% ~~or~~ of its side chain exposed to the surface (as defined in Example 1 herein).

34. (Currently amended) The full-length variant according to claim 33, wherein said cysteine residue is introduced in a position comprising an amino acid residue having at least 50% ~~or~~ of its side chain exposed to the surface (as defined in Example 1 herein).

35. (Currently amended) The full-length variant according to ~~any of~~ claim 32, wherein said cysteine residue is introduced by substitution.

36. (Currently amended) The full-length variant according to claim 32, wherein said up to 10 residue modifications is a substitution ~~is~~ selected from the group consisting of N10C, N16C, E38C, N59C, N83C, K94C, N104C and A124C.

37. (Original) The full-length variant according to claim 36, wherein said substitution is selected from the group consisting of N16C, N59C and N16C+N59C.

38. (Previously presented) The full-length variant of claim 32, wherein said cysteine residue is covalently attached to a polymer molecule.

39. (Original) The full-length variant according to claim 38, wherein said polymer molecule is a linear or branched polyethylene glycol.

40. (Previously presented) The full-length variant according to claim 22, wherein said up to 10 residue modifications comprises at least one introduced N-glycosylation site and at least one introduced cysteine residue.

41. (Cancelled)

42. (Currently amended) The full-length variant of claim 1, wherein said variant comprises an amino acid sequence from residue no. 1 to residue no. 131, which is identical to the amino acid sequence from residue no. 1 to residue no. 131 of huIFNG of SEQ ID NO: 1.

43. (Original) The full-length variant according to claim 42, wherein said variant is un-glycosylated.

44. (Previously presented) The full-length variant of claim 32, wherein said variant is glycosylated.

45. (Previously presented) A nucleotide sequence encoding the full-length variant of claim 1.

46. (Original) An expression vector comprising a nucleotide sequence as defined in claim 45.

47. (Previously presented) An isolated host cell comprising a nucleotide sequence as defined in claim 45 or an expression vector according to claim 46.

Claims 48-49 (Cancelled)

50. (Currently amended) A composition comprising a a full-length IFNG variant of claim 1 and a carrier.

51. (Previously presented) A pharmaceutical composition comprising a full-length variant of claim 1 and a pharmaceutically acceptable diluent, carrier or adjuvant.

Claims 52-58 (Cancelled)

59. (Previously presented) A method for producing a full-length IFNG polypeptide, said method comprising

i) cultivating a host cell as defined in claim 47 under conditions suitable for production of the IFNG polypeptide, and

ii) recovering the IFNG polypeptide.